



E4
<110> Dirk
Scanlan, Matthew
Gure, Ali
Jager, Elke
Knuth, Alexander
Old, Lloyd
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

<160> 19

<210> 1

<211> 1533

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 235

<223> unknown

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 cccgcggggg ctcgagaca gtttcaggcc gcattttgc tgaccgagg gtggggccgc 180
 gcgtggccgt ggaaacagat cctgaaggag ctagacgagt gctacgagcg cttcagtcgc 240
 gagacagacg gggcgagaa ggcggcgatg ctgcactgtg tgcagcgcg gctgatccgc 300
 agccaggagc tgggcgacga gaagatccag atcgtgagcc agatggtgga gctggtggag 360
 aaccgcagcg ggcagggtga cagccacgtg gagctgttcg aggcgcagca ggagctgggc 420
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 cagtctgaca agcccaacag caagcgctca cggcggcagc gcaacaacga gaaccgtgag 540
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 aca 1143

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 ggggcgcaga agcggcggat gctgcactgt gtgcagcgcg cgctgatccg cagccaggag 240
 ctgggcgacg agaagatcca gatcgtgagc cagatggtgg agctggtgga gaaccgcacg 300
 cggcaggtgg acagccacgt ggagctgttc gaggcgcagc aggagctggg cgacacagcg 360
 ggcaacagcg gcaaggctgg cgcggacagg cccaaaggcg aggcggcagc gcaggctgac 420
 aagcccaaca gcaagcgctc acggcggcag cgcaacaacg agaaccgtga gaacgcgtcc 480
 agcaaccacg accacgacga cggcgcctcg ggcacacca aggagaagaa ggccaagacc 540
 tccaagaaga agaagcgctc caaggccaag gcggagcgag aggcgtcccc tgccgacctc 600
 cccatcgacc ccaacgaacc cagtgactgt ctgtgcaacc aggtctccta tggggagatg 660
 atcggctgcg acaacgacga gtgccccatc gagtgggtcc acttctcgtg cgtggggctc 720
 aatcataaac ccaagggcaa gt 742

<210> 4
 <211> 857
 <212> DNA
 <213> Homo sapiens
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 ctttgtctcc aagccgttcc aaactgagta ccgggagacg acacaaaggg agggcggtga 180

cggatggcgc aggcgcggga gccgcctagg ctgctgggag tgggtgggccg gccgcggaat 240
 ggagatcctg aaggagctag acgagtgcta cgagcgcttc agtcgcgaga cagacggggc 300
 gcagaagcgg cggatgctgc actgtgtgca gcgcgcgctg atccgcagcc aggagctggg 360
 cgacgagaag atccagatcg tgagccagat ggtggagctg gtggagaacc gcacgcggca 420
 ggtggacagc cacgtggagc tgttcgaggc gcagcaggag ctgggcgaca cagcgggcaa 480
 cagcggcaag gctggcgcgg acaggcccaa aggcgaggcg gcagcgagc ctgacaagcc 540
 caacagcaag cgctcacggc ggcagcgcaa caacgagaac cgtgagaacg cgtccagcaa 600
 ccacgaccac gacgagggcg cctcgggcac acccaaggag aagaaggcca agacctccaa 660
 gaagaagaag cgctccaagg ccaaggcgga gcgagaggcg tcccctgccg acctcccat 720
 cgaccccaac gaaccacgt actgtctgtg caaccaggtc tcctatgggg agatgatcgg 780
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<211> 279

<212> PRT

<213> Homo sapiens

<400> 5

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Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
20 25 30

Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
35 40 45

Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
50 55 60

Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
65 70 75 80

Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
85 90 95

Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
100 105 110

Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys
115 120 125

Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys
130 135 140

Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
 145 150 155 160
 Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
 165 170 175
 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
 180 185 190
 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
 195 200 205
 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
 210 215 220
 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
 225 230 235 240
 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
 245 250 255
 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
 260 265 270
 Lys Glu Arg Ala Tyr Asn Arg
 275

<210> 6
 <211> 210
 <212> PRT
 <213> Homo sapiens
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 <400> 6

Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser Gln Glu Leu Gly
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 Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu Val Glu Asn
 20 25 30
 Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln
 35 40 45
 Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
 50 55 60
 Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
 65 70 75 80
 Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn
 85 90 95
 His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala
 100 105 110
 Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
 115 120 125

Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
130 135 140

Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
145 150 155 160

Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
165 170 175

Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg Gly Glu Asn Glu
180 185 190

Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys Glu Arg Ala Tyr
195 200 205

Asn Arg
210

<210> 7

<211> 235

<212> PRT

<213> Homo sapiens

<400> 7

Met Glu Ile Leu Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg
1 5 10 15

Glu Thr Asp Gly Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg
20 25 30

Ala Leu Ile Arg Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val
35 40 45

Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
50 55 60

His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
65 70 75 80

Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
85 90 95

Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
100 105 110

Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
115 120 125

Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys
130 135 140

Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro
145 150 155 160

Ile Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr
165 170 175

Gly Glu Met Ile Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe
 180 185 190

His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr
 195 200 205

Cys Pro Lys Cys Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu
 210 215 220

Glu Lys Ser Lys Lys Glu Arg Ala Tyr Asn Arg
 225 230 235

<210> 8

<211> 772

<212> DNA

<213> Homo sapiens

<221> CDS

<222> 689,714

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 ccagcgagcc ctctactgg gagatgatcc gctgcgacaa cgaatgcccc atcgagtggg 240
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 gccggggaaa gaacgatggg caaagccctt gagaagtcca gaaaaaaaaac agggcttata 360
 acaggtagtt tggggacatg cgtctaata tagaggagaac aaaataagcc agtgtgttga 420
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 tactaaaaat tcaaaaaaaaa aattagctgg gcgtggtggc gggcgctgt agtcccagct 660
 attcgggagg ctgaggcagg agaatggcnt gaacctggga ggtggagctt gcantgagcc 720
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<210> 9

<211> 32

<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 23
<212> DNA
<213> Homo sapiens
<400> 10
cgtggtcgtg gttgctggac gcg 23

<210> 11
<211> 21
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<213> Homo sapiens
<400> 11
cccagcggcc ctgacgctgt c 21

<210> 12
<211> 23
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<213> Homo sapiens
<400> 12
cgtggtcgtg gttgctggac gcg 23

<210> 13
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<213> Homo sapiens
<400> 13
ggaagagata aggcctaggg aag 23

<210> 14
<211> 23
<212> DNA
<213> Homo sapiens
<400> 14
cgtggtcgtg gttgctggac gcg 23

<210> 15
<211> 2030
<212> DNA
<213> Homo sapiens
<221> CDS
<222> 1628, 1752, 1758, 1769, 1789, 1873, 1908, 1915, 1933, 1970, 1976, 2022
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ctcctgataa tgatggtttt ctgaaggctc cctgcagaat gaaagtttct attccaacta 420
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tcatgcacat aangaaagct gacaacaaaa gcaagataac aattgatntt cattntcttg 1920
agaggaaaat gcncatcatc ttctaaaaga gaaaaatgag gagatatttn attacnataa 1980
ccatttaaaa aaccctgata tttcaatatg gaaaaaaaaa anaaaaaaaaa 2030

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 <211> 512
 <212> PRT
 <213> Homo sapiens
 <400> 16
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 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 35 40 45
 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 50 55 60
 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 65 70 75 80
 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
 85 90 95
 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
 100 105 110
 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
 115 120 125
 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
 130 135 140
 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 145 150 155 160
 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
 165 170 175
 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
 180 185 190
 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
 195 200 205
 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
 210 215 220
 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
 225 230 235 240
 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
 245 250 255
 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
 260 265 270
 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp

275					280					285				
Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu
290						295					300			
Lys	Arg	Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu
305					310					315				320
Gly	Arg	Ile	Glu	Glu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln
			325						330					335
Leu	Glu	Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val
			340					345					350	
Ser	Asn	Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr
	355						360				365			
Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys
	370					375					380			
Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys
385						390					395			400
Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln
			405					410						415
Thr	Leu	Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln
			420					425					430	
Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr
	435						440					445		
Lys	Leu	Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu	Ala	Glu	Ile
	450					455					460			
Ser	His	His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp	His	Asp	Gln
465						470					475			480
Val	Thr	Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His	Ile	Ala	Gly
			485					490						495
Ala	Cys	Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser	Ser	Thr	Asp
			500					505					510	

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 <400> 17
 cacacaggat ccatgcaggc cccgcacaag gag 33

<210> 18
 <211> 34
 <212> DNA
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<400> 18
cacacaaagc ttctaggatt tggcacagcc agag 34

<210> 19
<211> 294
<212> PRT
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Met Pro Leu Cys Thr Ala Thr Arg Ile Pro Arg Tyr Ser Ser Ser Ser
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Asp Pro Gly Pro Val Ala Arg Gly Arg Gly Cys Ser Ser Asp Arg Leu
20 25 30

Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Leu
35 40 45

Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys
50 55 60

Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
65 70 75 80

Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
85 90 95

Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
100 105 110

Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
115 120 125

Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
130 135 140

Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
145 150 155 160

Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
165 170 175

Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
180 185 190

Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys
195 200 205

Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu
210 215 220

Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
225 230 235 240

Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
245 250 255

Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
260 265 270

Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
275 280 285

Glu Arg Ala Tyr Asn Arg
290 294

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E4

Conclude

